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**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/186,269A**DATE: 09/08/94
TIME: 17:28:05*INPUT SET: S3560.raw*

**This Raw Listing contains the General
Information Section and up to the first 5 pages.**

X6
ENTERED

1 SEQUENCE LISTING
2
3 (1) General Information:
4
5 (i) APPLICANT: Bendig, Mary M.
6 Leger, Olivier J.
7 Saldanha, Jose
8 Jones, S. Tarran
9
10 (ii) TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
11 Adhesion Molecule VLA-4
12
13 (iii) NUMBER OF SEQUENCES: 45
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Townsend and Townsend Khourie and Crew
17 (B) STREET: One Market Plaza, Steuart Tower, Suite 2000
18 (C) CITY: San Francisco
19 (D) STATE: California
20 (E) COUNTRY: USA
21 (F) ZIP: 94105
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 08/186,269
31 (B) FILING DATE: 25-JAN-1994
32 (C) CLASSIFICATION:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Smith, William L.
36 (B) REGISTRATION NUMBER: 30,223
37 (C) REFERENCE/DOCKET NUMBER: 15270-14
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 415-543-9600
41 (B) TELEFAX: 415-543-5043
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

**RAW SEQUENCE LISTING
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47 (A) LENGTH: 483 base pairs
 48 (B) TYPE: nucleic acid
 49 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

51
 52 (ii) MOLECULE TYPE: cDNA
 53

54
 55 (ix) FEATURE:
 56 (A) NAME/KEY: CDS
 57 (B) LOCATION: 53..430
 58

59
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

62 ATGAGGGCCC CTGCTCAGAT TTTTGGATT TTGGTCAGGA GACGTTGTAG AA ATG	55
63	Met
64	1
65	
66 AGA CCG TCT ATT CAG TTC CTG GGG CTC TTG TTG TTC TGG CTT CAT GGT	103
67 Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Phe Trp Leu His Gly	
68 5 10 15	
69	
70 GCT CAG TGT GAC ATC CAG ATG ACA CAG TCT CCA TCC TCA CTG TCT GCA	151
71 Ala Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
72 20 25 30	
73	
74 TCT CTG GGA GGC AAA GTC ACC ATC ACT TGC AAG ACA AGC CAA GAC ATT	199
75 Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Thr Ser Gln Asp Ile	
76 35 40 45	
77	
78 AAC AAG TAT ATG GCT TGG TAC CAA CAC AAG CCT GGA AAA CGT CCT AGG	247
79 Asn Lys Tyr Met Ala Trp Tyr Gln His Lys Pro Gly Lys Arg Pro Arg	
80 50 55 60 65	
81	
82 CTG CTC ATA CAT TAC ACA TCT GCA TTA CAG CCA GGC ATC CCA TCA AGG	295
83 Leu Leu Ile His Tyr Thr Ser Ala Leu Gln Pro Gly Ile Pro Ser Arg	
84 70 75 80	
85	
86 TTC AGT GGA AGT GGG TCT GGG AGA GAT TAT TCC TTC AAC ATC AGC AAC	343
87 Phe Ser Gly Ser Gly Arg Asp Tyr Ser Phe Asn Ile Ser Asn	
88 85 90 95	
89	
90 CTG GAG CCT GAA GAT ATT GCA ACT TAT TAT TGT CTA CAG TAT GAT AAT	391
91 Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn	
92 100 105 110	
93	
94 CTG TGG ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGGGCTGATG	440
95 Leu Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys	
96 115 120 125	
97	
98 CTGCACCAAC TGTATCCATC TTCCCCACCAT CCACCCGGGA TCC	483
99	

**RAW SEQUENCE LISTING
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100 (2) INFORMATION FOR SEQ ID NO:2:

101

102 (i) SEQUENCE CHARACTERISTICS:
103 (A) LENGTH: 126 amino acids
104 (B) TYPE: amino acid
105 (D) TOPOLOGY: linear

106

107 (ii) MOLECULE TYPE: protein

108

109 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

110

111 Met Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His
112 1 5 10 15

113

114 Gly Ala Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
115 20 25 30

116

117 Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Thr Ser Gln Asp
118 35 40 45

119

120 Ile Asn Lys Tyr Met Ala Trp Tyr Gln His Lys Pro Gly Lys Arg Pro
121 50 55 60

122

123 Arg Leu Leu Ile His Tyr Thr Ser Ala Leu Gln Pro Gly Ile Pro Ser
124 65 70 75 80

125

126 Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Asn Ile Ser
127 85 90 95

128

129 Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
130 100 105 110

131

132 Asn Leu Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
133 115 120 125

134

135

136 (2) INFORMATION FOR SEQ ID NO:3:

137

138 (i) SEQUENCE CHARACTERISTICS:
139 (A) LENGTH: 470 base pairs
140 (B) TYPE: nucleic acid
141 (C) STRANDEDNESS: double
142 (D) TOPOLOGY: linear

143

144 (ii) MOLECULE TYPE: cDNA

145

146

147 (ix) FEATURE:
148 (A) NAME/KEY: CDS
149 (B) LOCATION: 1..420

150

151

152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

**RAW SEQUENCE LISTING
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153				
154	ATG AAA TGC AGC TGG GTC ATG TTC TTC CTG ATG GCA GTG GTT ACA GGG			48
155	Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly			
156	1 5 10 15			
157				
158	GTC AAT TCA GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG			96
159	Val Asn Ser Glu Val Gln Leu Gln Ser Gly Ala Glu Leu Val Lys			
160	20 25 30			
161				
162	CCA GGG GCC TCA GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT			144
163	Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile			
164	35 40 45			
165				
166	AAA GAC ACC TAT ATA CAC TGT GTG AAG CAG AGG CCT GAA CAG GGC CTG			192
167	Lys Asp Thr Tyr Ile His Cys Val Lys Gln Arg Pro Glu Gln Gly Leu			
168	50 55 60			
169				
170	GAG TGG ATT GGA AGG ATT GAT CCT GCG AAT GGT TAT ACT AAA TAT GAC			240
171	Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Tyr Thr Lys Tyr Asp			
172	65 70 75 80			
173				
174	CCG AAG TTC CAG GGC AAG GCC ACT ATA ACA GCT GAC ACA TCC TCC AAC			288
175	Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn			
176	85 90 95			
177				
178	ACA GCC TAC CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC			336
179	Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val			
180	100 105 110			
181				
182	TAT TTC TGT GCT AGA GAG GGA TAT TAT GGT AAC TAC GGG GTC TAT GCT			384
183	Tyr Phe Cys Ala Arg Glu Gly Tyr Tyr Gly Asn Tyr Gly Val Tyr Ala			
184	115 120 125			
185				
186	ATG GAC TAC TGG GGT CAA GGA ACC TCA GTC ACC GTC TCCTCAGCCA			430
187	Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val			
188	130 135 140			
189				
190	AAACGACACC CCCATCTGTC TATCCACTGG CCCGGGATCC			470
191				
192				
193	(2) INFORMATION FOR SEQ ID NO:4:			
194				
195	(i) SEQUENCE CHARACTERISTICS:			
196	(A) LENGTH: 140 amino acids			
197	(B) TYPE: amino acid			
198	(D) TOPOLOGY: linear			
199				
200	(ii) MOLECULE TYPE: protein			
201				
202	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:			
203				
204	Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly			
205	1 5 10 15			

**RAW SEQUENCE LISTING
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206
207 Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
208 20 25 30
209
210 Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
211 35 40 45
212
213 Lys Asp Thr Tyr Ile His Cys Val Lys Gln Arg Pro Glu Gln Gly Leu
214 50 55 60
215
216 Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Tyr Thr Lys Tyr Asp
217 65 70 75 80
218
219 Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
220 85 90 95
221
222 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
223 100 105 110
224
225 Tyr Phe Cys Ala Arg Glu Gly Tyr Tyr Gly Asn Tyr Gly Val Tyr Ala
226 115 120 125
227
228 Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
229 130 135 140
230
231 (2) INFORMATION FOR SEQ ID NO:5:
232
233 (i) SEQUENCE CHARACTERISTICS:
234 (A) LENGTH: 106 amino acids
235 (B) TYPE: amino acid
236 (C) STRANDEDNESS: single
237 (D) TOPOLOGY: linear
238
239 (ii) MOLECULE TYPE: protein
240
241
242
243 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
244
245 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
246 1 5 10 15
247
248 Gly Lys Val Thr Ile Thr Cys Lys Thr Ser Gln Asp Ile Asn Lys Tyr
249 20 25 30
250
251 Met Ala Trp Tyr Gln His Lys Pro Gly Lys Arg Pro Arg Leu Leu Ile
252 35 40 45
253
254 His Tyr Thr Ser Ala Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
255 50 55 60
256
257 Ser Gly Ser Gly Arg Asp Tyr Ser Phe Asn Ile Ser Asn Leu Glu Pro
258 65 70 75 80

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SEQUENCE VERIFICATION REPORT
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